

SEQUENCE LISTING

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Institute National de la Recherche Agronomique

<120> YEAST STRAINS WITH IMPROVED FRUCTOSE FERMENTATION CAPACITY

<130> 21568WO

<150> EP 03078992.9
<151> 2003-12-19

<160> 30

<170> PatentIn version 3.1

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 <213> *Saccharomyces cerevisiae*

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aagaaaatgt tcggcaagaa ataa 1704

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<210> 26
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<212> PRT
<213> Saccharomyces cerevisiae

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<400> 26

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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro
20          25          30

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Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
35          40          45

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Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
50          55          60

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Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65          70          75          80

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Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
85          90          95

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Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
100         105         110

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Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
180 185 190

Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
195 200 205

Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly

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 Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
 370 375 380
 Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val
 385 390 395 400
 Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn
 405 410 415
 Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
 420 425 430
 Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
 435 440 445
 Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
 450 455 460
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 465 470 475 480
 Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
 485 490 495
 Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
 500 505 510
 Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
 515 520 525
 Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
 530 535 540
 Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
 545 550 555 560
 Lys Lys Met Phe Gly Lys Lys
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<210> 27
 <211> 567
 <212> PRT
 <213> Mutated HXT3 protein

<400> 27

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Met Asn Ser Thr Pro Asp Leu Ile Ser Pro Gln Lys Ser Ser Glu Asn
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Ser Asn Ala Asp Leu Pro Ser Asn Ser Ser Gln Val Met Asn Met Pro
          20          25          30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
          35          40          45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
          50          55          60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
65          70          75          80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
          85          90          95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
          100          105          110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
          115          120          125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
          130          135          140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
          145          150          155          160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
          165          170          175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
          180          185          190

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Ala Pro Lys Glu Met Arg Gly Thr Leu Val Ser Cys Tyr Gln Leu Met
195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305 310 315 320

Arg Thr Met Met Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
370 375 380

Asn Cys Leu Leu Tyr Gly Ala Ile Gly Met Val Cys Cys Tyr Val Val
385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Glu Gly Asn
405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe

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420 425 430
 Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val
 435 440 445
 Ile Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
 450 455 460
 Ala Thr Ala Ala Asn Trp Leu Trp Gly Phe Leu Ile Gly Phe Phe Thr
 465 470 475 480
 Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
 485 490 495
 Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
 500 505 510
 Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
 515 520 525
 Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
 530 535 540
 Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
 545 550 555 560
 Lys Lys Met Phe Gly Lys Lys
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<210> 28

<211> 1704

<212> DNA

<213> Mutated HXT3 gene

<400> 28

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 aaagatggta gttattattt gtctaagggtt agaactgggt taattgtctc cattttcaac 360

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aagaaaatgt tcggcaagaa ataa 1704

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<210> 29

<211> 1704

<212> DNA

<213> Mutated HXT3 gene II

<400> 29

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aagaaaatgt tcggcaagaa ataa 1704

<210> 30

<211> 567

<212> PRT

<213> Mutated HXT3 protein II

<400> 30

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 20 25 30

Glu Glu Lys Gly Val Gln Asp Asp Phe Gln Ala Glu Ala Asp Gln Val
 35 40 45

Leu Thr Asn Pro Asn Thr Gly Lys Gly Ala Tyr Val Thr Val Ser Ile
 50 55 60

Cys Cys Val Met Val Ala Phe Gly Gly Phe Val Phe Gly Trp Asp Thr
 65 70 75 80

Gly Thr Ile Ser Gly Phe Val Ala Gln Thr Asp Phe Leu Arg Arg Phe
 85 90 95

Gly Met Lys His Lys Asp Gly Ser Tyr Tyr Leu Ser Lys Val Arg Thr
 100 105 110

Gly Leu Ile Val Ser Ile Phe Asn Ile Gly Cys Ala Ile Gly Gly Ile
 115 120 125

Ile Leu Ala Lys Leu Gly Asp Met Tyr Gly Arg Lys Met Gly Leu Ile
 130 135 140

Val Val Val Val Ile Tyr Ile Ile Gly Ile Ile Ile Gln Ile Ala Ser
 145 150 155 160

Ile Asn Lys Trp Tyr Gln Tyr Phe Ile Gly Arg Ile Ile Ser Gly Leu
 165 170 175

Gly Val Gly Gly Ile Ala Val Leu Ser Pro Met Leu Ile Ser Glu Val
 180 185 190

Ala Pro Lys Glu Met Arg Gly Ala Leu Val Ser Cys Tyr Gln Leu Met
 195 200 205

Val Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Asn Phe Gly Thr Lys
210 215 220

Asn Tyr Ser Asn Ser Val Gln Trp Arg Val Pro Leu Gly Leu Cys Phe
225 230 235 240

Ala Trp Ala Leu Phe Met Ile Gly Gly Met Thr Phe Val Pro Glu Ser
245 250 255

Pro Arg Tyr Leu Val Glu Ala Gly Gln Ile Asp Glu Ala Arg Ala Ser
260 265 270

Leu Ser Lys Val Asn Lys Val Ala Pro Asp His Pro Phe Ile Gln Gln
275 280 285

Glu Leu Glu Val Ile Glu Ala Ser Val Glu Glu Ala Arg Ala Ala Gly
290 295 300

Ser Ala Ser Trp Gly Glu Leu Phe Thr Gly Lys Pro Ala Met Phe Lys
305 310 315 320

Arg Thr Met Ile Gly Ile Met Ile Gln Ser Leu Gln Gln Leu Thr Gly
325 330 335

Asp Asn Tyr Phe Phe Tyr Tyr Gly Thr Thr Val Phe Asn Ala Val Gly
340 345 350

Met Ser Asp Ser Phe Glu Thr Ser Ile Val Phe Gly Val Val Asn Phe
355 360 365

Phe Ser Thr Cys Cys Ser Leu Tyr Thr Val Asp Arg Phe Gly Arg Arg
370 375 380

Asn Cys Leu Met Trp Gly Ala Val Gly Met Val Cys Cys Tyr Val Val
385 390 395 400

Tyr Ala Ser Val Gly Val Thr Arg Leu Trp Pro Asn Gly Gln Asn Asn
405 410 415

Gly Ser Ser Lys Gly Ala Gly Asn Cys Met Ile Val Phe Ala Cys Phe
420 425 430

Tyr Ile Phe Cys Phe Ala Thr Thr Trp Ala Pro Ile Ala Tyr Val Val

435 440 445

Val Ser Glu Thr Phe Pro Leu Arg Val Lys Ser Lys Ala Met Ser Ile
450 455 460

Ala Thr Ala Ala Asn Trp Ile Trp Gly Phe Leu Ile Gly Phe Phe Thr
465 470 475 480

Pro Phe Ile Thr Gly Ala Ile Asn Phe Tyr Tyr Gly Tyr Val Phe Met
 485 490 495

Gly Cys Met Val Phe Ala Tyr Phe Tyr Val Phe Phe Phe Val Pro Glu
 500 505 510

Thr Lys Gly Leu Thr Leu Glu Glu Val Asn Asp Met Tyr Ala Glu Gly
515 520 525

Val Leu Pro Trp Lys Ser Ala Ser Trp Val Pro Thr Ser Gln Arg Gly
530 535 540

Ala Asn Tyr Asp Ala Asp Ala Leu Met His Asp Asp Gln Pro Phe Tyr
545 550 555 560

Lys Lys Met Phe Gly Lys Lys
565